

Sequence ID No. 1

Sequence Length: 316

Sequence Type: amino acid

Strandedness: 1

Topology: linear

Molecule Type: protein

Sequence:

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser
1				5					10					15
Glu	Glu	Met	Gly	Ser	Gly	Pro	Gly	Val	Pro	His	Glu	Gly	Pro	Leu
				20					25					30
His	Pro	Ala	Pro	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala
				35					40					45
Ser	Arg	Ser	Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln
				50					55					60
Val	Val	Cys	Ser	Ile	Ala	Leu	Phe	Leu	Tyr	Phe	Arg	Ala	Gln	Met
				65					70					75
Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg
				80					85					90
Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr	Leu
				95					100					105

09202455.121598

Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln			
110	115	120	
Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly			
125	130	135	
Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp			
140	145	150	
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala			
155	160	165	
His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys			
170	175	180	
Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile			
185	190	195	
Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp			
200	205	210	
Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu			
215	220	225	
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr			
230	235	240	
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met			
245	250	255	
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His			
260	265	270	
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly			
275	280	285	

Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro

290

295

300

Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile

305

310

315

Asp

316

Sequence ID No. 2

Sequence Length: 1538

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: cDNA to mRNA

Sequence:

GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG 60
TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CCGGGCGCCG 120
CGCCATGCGC CGGGCCAGCC GAGACTACGG CAAGTACCTG CGCAGCTCGG AGGAGATGGG 180
CAGCGGCCCC GCGGTCCCAC ACGAGGGTCC GCTGCACCCC GCGCCTTCTG CACCGGCTCC 240
GGCGCCGCCA CCCGCCGCCT CCCGCTCCAT GTTCCTGGCC CTCCTGGGGC TGGGACTGGG 300
CCAGGTGGTC TGCAGCATCG CTCTGTTCTT GTACTTTTCA GCGCAGATGG ATCCTAACAG 360
AATATCAGAA GACAGCACTC ACTGCTTTTA TAGAATCCTG AGACTCCATG AAAACGCAGG 420
TTTGCAGGAC TCGACTCTGG AGAGTGAAGA CACACTACCT GACTCCTGCA GGAGGATGAA 480
ACAAGCCTTT CAGGGGGCCG TGCAGAAGGA ACTGCAACAC ATTGTGGGGC CACAGCGCTT 540
CTCAGGAGCT CCAGCTATGA TGGAAGGCTC ATGGTTGGAT GTGGCCCAGC GAGGCAAGCC 600

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TGAGGCCCAG CCATTTGCAC ACCTCACCAT CAATGCTGCC AGCATCCCAT CGGGTTCCCA 660
TAAAGTCACT CTGTCCTCTT GGTACCACGA TCGAGGCTGG GCCAAGATCT CTAACATGAC 720
GTTAAGCAAC GGAAACTAA GGGTTAACCA AGATGGCTTC TATTACCTGT ACGCCAACAT 780
TTGCTTTCGG CATCATGAAA CATCGGGAAG CGTACCTACA GACTATCTTC AGCTGATGGT 840
GTATGTCGTT AAAACCAGCA TCAAAATCCC AAGTTCTCAT AACCTGATGA AAGGAGGGAG 900
CAGGAAAAAC TGGTCGGGCA ATTCTGAATT CCACTTTTAT TCCATAAATG TTGGGGGATT 960
TTTCAAGCTC CGAGCTGGTG AAGAAATTAG CATTGAGGTG TCCAACCCTT CCCTGCTGGA 1020
TCCGGATCAA GATGCGACGT ACTTTGGGGC TTTCAAAGTT CAGGACATAG ACTGAGACTC 1080
ATTTCTGTTG ACATTAGCAT GGATGTCCTA GATGTTTGGA AACTTCTTAA AAAATGGATG 1140
ATGTCTATAC ATGTGTAAGA CTACTAAGAG ACATGGCCCA CGGTGTATGA AACTCACAGC 1200
CCTCTCTCTT GAGCCTGTAC AGGTTGTGTA TATGTAAAGT CCATAGGTGA TGTTAGATTC 1260
ATGGTGATTA CACAACGGTT TTACAATTTT GTAATGATTT CCTAGAATTG AACCAGATTG 1320
GGAGAGGTAT TCCGATGCTT ATGAAAAACT TACACGTGAG CTATGGAAGG GGGTCACAGT 1380
CTCTGGGTCT AACCCTGGA CATGTGCCAC TGAGAACCTT GAAATTAAGA GGATGCCATG 1440
TCATTGCAAA GAAATGATAG TGTGAAGGGT TAAGTTCTTT TGAATTGTTA CATTGCGCTG 1500
GGACCTGCAA ATAAGTTCTT TTTTCTAAT GAGGAGAG 1538

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Sequence ID No. 3

Sequence Length: 21

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

AAACGCAAAA AACCAGAAAG G

21

Sequence ID No. 4

Sequence Length: 17

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

GTAAAACGAC GGCCAGT

17

Sequence ID No. 5

Sequence Length: 17

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

CAGGAAACAG CTATGAC

17

Sequence ID No. 6

Sequence Length: 22

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

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Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

AAGCCCCAAA GTACGTCGCA TC

22

Sequence ID No. 7

Sequence Length: 26

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

CGAAGCTTTC GAGCGCAGAT GGATCC

26

Sequence ID No. 8

Sequence Length: 27

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

CCTCTAGAGT CTATGTCCTG AAGTTTG

27

Sequence ID No. 9

Sequence Length: 20

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Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

ATCAGAAGAC AGCACTCACT

20

Sequence ID No. 10

Sequence Length: 33

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

GGGGTCGACC TAGGACATCC ATGCTAATGT TCC 33

Sequence ID No. 11

Sequence Length: 317

Sequence Type: amino acid

Strandedness: 1

Topology: linear

Molecule Type: protein

Sequence:

0920455.124598
865727.55420260

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu
				5					10					15	
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala
				20					25					30	
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met
				35					40					45	
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val
				50					55					60	
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser
65						70				75				80	
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn
						85				90				95	
Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile
						100				105				110	
Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln
						115				120				125	
Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys
						130				135				140	
Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu
145										150				155	160
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro
						165				170				175	
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly
						180				185				190	

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Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220
His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240
Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
245 250 255
Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285
Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
290 295 300
Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

Sequence ID No. 12

Sequence Length: 954

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: cDNA to mRNA

Sequence:

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ATGCGCCGCG CCAGCAGAGA CTACACCAAG TACCTGCGTG GCTCGGAGGA GATGGGCGGC 60
GGCCCCGGAG CCCCACGA GGGCCCCCTG CACGCCCCGC CGCCGCCTGC GCCGCACCAG 120
CCCCCTGCCG CCTCCCGCTC CATGTTTCGTG GCCCTCCTGG GGCTGGGGCT GGGCCAGGTT 180
GTCTGCAGCG TCGCCCTGTT CTTCTATTTT AGAGCGCAGA TGGATCCTAA TAGAATATCA 240
GAAGATGGCA CTCACTGCAT TTATAGAATT TTGAGACTCC ATGAAAATGC AGATTTTCAA 300
GACACAACCTC TGGAGAGTCA AGATACAAAA TTAATACCTG ATTCATGTAG GAGAATTAAA 360
CAGGCCTTTC AAGGAGCTGT GCAAAAGGAA TTACAACATA TCGTTGGATC ACAGCACATC 420
AGAGCAGAGA AAGCGATGGT GGATGGCTCA TGGTTAGATC TGGCCAAGAG GAGCAAGCTT 480
GAAGCTCAGC CTTTTGCTCA TCTCACTATT AATGCCACCG ACATCCCATC TGGTTCCCAT 540
AAAGTGAGTC TGTCTCTTG GTACCATGAT CGGGGTGGG CCAAGATCTC CAACATGACT 600
TTTAGCAATG GAAAACTAAT AGTTAATCAG GATGGCTTTT ATTACCTGTA TGCCAACATT 660
TGCTTTTCGAC ATCATGAAAC TTCAGGAGAC CTAGCTACAG AGTATCTTCA ACTAATGGTG 720
TACGTCACTA AAACCAGCAT CAAAATCCCA AGTTCTCATA CCCTGATGAA AGGAGGAAGC 780
ACCAAGTATT GGTGAGGAA TTCTGAATTC CATTTTTATT CCATAAACGT TGGTGGATTT 840
TTTAAGTTAC GGTCTGGAGA GGAAATCAGC ATCGAGGTCT CCAACCCCTC CTTACTGGAT 900
CCGGATCAGG ATGCAACATA CTTTGGGGCT TTAAAGTTC GAGATATAGA TTGA 954
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Sequence ID No. 13

Sequence Length: 27

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

GGCGTACGCA GAGCGCAGAT GGATCCT

27

Sequence ID No. 14

Sequence Length: 34

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: other nucleic acid (synthetic DNA)

Sequence:

GGGGTCGACC ATCCAGGAAA TATCATAACA CTCC 34

Sequence ID No. 15

Sequence Length: 951

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: cDNA to mRNA

Sequence:

ATGCCCGGG CCAGCCGAGA CTACGGCAAG TACCTGCGCA GCTCGGAGGA GATGGGCAGC 60
GGCCCCGGCG TCCCACACGA GGGTCCGCTG CACCCCGCGC CTTCTGCACC GGCTCCGGCG 120
CCGCCACCCG CCGCTCCCG CTCCATGTTT CTGGCCCTCC TGGGGCTGGG ACTGGGCCAG 180
GTGGTCTGCA GCATCGCTCT GTTCTGTAC TTTCCAGCGC AGATGGATCC TAACAGAATA 240
TCAGAAGACA GCACTCACTG CTTTATAGA ATCCTGAGAC TCCATGAAAA CGCAGGTTTG 300
CAGGACTCGA CTCTGGAGAG TGAAGACACA CTACCTGACT CCTGCAGGAG GATGAAACAA 360
GCCTTTCAGG GGGCCGTGCA GAAGGAACTG CAACACATTG TGGGGCCACA GCGCTTCTCA 420

GGAGCTCCAG CTATGATGGA AGGCTCATGG TTGGATGTGG CCCAGCGAGG CAAGCCTGAG 480
 GCCCAGCCAT TTGCACACCT CACCATCAAT GCTGCCAGCA TCCCATCGGG TTCCCATAAA 540
 GTCACTCTGT CCTCTTGGA CCACGATCGA GGCTGGGCCA AGATCTCTAA CATGACGTTA 600
 AGCAACGGAA AACTAAGGGT TAACCAAGAT GGCTTCTATT ACCTGTACGC CAACATTTGC 660
 TTTCGGCATC ATGAAACATC GGAAGCGTA CCTACAGACT ATCTTCAGCT GATGGTGTAT 720
 GTCGTTAAAA CCAGCATCAA AATCCCAAGT TCTCATAACC TGATGAAAGG AGGGAGCACG 780
 AAAAAGTGGT CGGGCAATTC TGAATTCCAC TTTTATTCCA TAAATGTTGG GGGATTTTTC 840
 AAGCTCCGAG CTGGTGAAGA AATTAGCATT CAGGTGTCCA ACCCTTCCCT GCTGGATCCG 900
 GATCAAGATG CGACGTAATT TGGGGCTTTC AAAGTTCAGG ACATAGACTG A 951

Sequence ID No. 16

Sequence Length: 244

Sequence Type: amino acid

Strandedness: 1

Topology: linear

Molecule Type: protein

Sequence:

Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	His	Cys	Phe
1				5				10					15		
Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr
			20					25					30		
Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln
			35					40					45		

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Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro
50 55 60
Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp
65 70 75 80
Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr
85 90 95
Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser
100 105 110
Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu
115 120 125
Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr
130 135 140
Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr
145 150 155 160
Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile
165 170 175
Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser
180 185 190
Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe
195 200 205
Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser
210 215 220
Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val
225 230 235 240

Gln Asp Ile Asp

Sequence ID No. 17

Sequence Length: 246

Sequence Type: amino acid

Strandedness: 1

Topology: linear

Molecule Type: protein

Sequence:

Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile
1 5 10 15
Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr
20 25 30
Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile
35 40 45
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
50 55 60
Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp
65 70 75 80
Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His
85 90 95
Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser
100 105 110
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met

115	120	125
Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr		
130	135	140
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu		
145	150	155
Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile		
165	170	175
Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr		
180	185	190
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly		
195	200	205
Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn		
210	215	220
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe		
225	230	235
Lys Val Arg Asp Ile Asp		
245		

Sequence ID No. 18

Sequence Length: 735

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: cDNA to mRNA

Sequence:

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GCGCAGATGG ATCCTAACAG AATATCAGAA GACAGCACTC ACTGCTTTTA TAGAATCCTG   60
AGACTCCATG AAAACGCAGG TTTGCAGGAC TCGACTCTGG AGAGTGAAGA CACACTACCT  120
GACTCCTGCA GGAGGATGAA ACAAGCCTTT CAGGGGGCCG TGCAGAAGGA ACTGCAACAC  180
ATTGTGGGGC CACAGCGCTT CTCAGGAGCT CCAGCTATGA TGAAGGCTC ATGGTTGGAT  240
GTGGCCCAGC GAGGCAAGCC TGAGGCCAG CCATTTGCAC ACCTCACCAT CAATGCTGCC  300
AGCATCCCAT CGGGTTCCCA TAAAGTCACT CTGTCTCTT GGTACCACGA TCGAGGCTGG  360
GCCAAGATCT CTAACATGAC GTTAAGCAAC GGAAACTAA GGGTTAACCA AGATGGCTTC  420
TATTACCTGT ACGCCAACAT TTGCTTTCGG CATCATGAAA CATCGGGAAG CGTACCTACA  480
GACTATCTTC AGCTGATGGT GTATGTCGTT AAAACCAGCA TCAAAATCCC AAGTTCTCAT  540
AACCTGATGA AAGGAGGGAG CACGAAAAAC TGGTCGGGCA ATTCTGAATT CCACTTTTAT  600
TCCATAAATG TTGGGGGATT TTTCAAGCTC CGAGCTGGTG AAGAAATTAG CATTCAAGTG  660
TCCAACCCTT CCCTGCTGGA TCCGGATCAA GATGCGACGT ACTTTGGGGC TTTCAAAGTT  720
CAGGACATAG ACTGA                                                    735

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Sequence ID No. 19

Sequence Length: 741

Sequence Type: nucleic acid

Strandedness: 1

Topology: linear

Molecule Type: cDNA to mRNA

Sequence:

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GCGCAGATGG ATCCTAATAG AATATCAGAA GATGGCACTC ACTGCATTTA TAGAATTTTG   60
AGACTCCATG AAAATGCAGA TTTTCAAGAC ACAACTCTGG AGAGTCAAGA TACAAAATTA  120

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ATACCTGATT CATGTAGGAG AATTAAACAG GCCTTTCAAG GAGCTGTGCA AAAGGAATTA 180
CAACATATCG TTGGATCACA GCACATCAGA GCAGAGAAAG CGATGGTGGA TGGCTCATGG 240
TTAGATCTGG CCAAGAGGAG CAAGCTTGAA GCTCAGCCTT TTGCTCATCT CACTATTAAT 300
GCCACCGACA TCCCATCTGG TTCCCATAAA GTGAGTCTGT CCTCTTGGTA CCATGATCGG 360
GGTTGGGCCA AGATCTCCAA CATGACTTTT AGCAATGGAA AACTAATAGT TAATCAGGAT 420
GGCTTTTATT ACCTGTATGC CAACATTTGC TTTGACATC ATGAAACTTC AGGAGACCTA 480
GCTACAGAGT ATCTTCAACT AATGGTGTAC GTCATAAAA CCAGCATCAA AATCCCAAGT 540
TCTCATACCC TGATGAAAGG AGGAAGCACC AAGTATTGGT CAGGGAATTC TGAATTCCAT 600
TTTTATTCCA TAAACGTTGG TGGATTTTTT AAGTTACGGT CTGGAGAGGA AATCAGCATC 660
GAGGTCTCCA ACCCCTCCTT ACTGGATCCG GATCAGGATG CAACATACTT TGGGGCTTTT 720
AAAGTTCGAG ATATAGATTG A 741